

SEQUENCE LISTING

<110> RIKEN

<120> Truncated Reelin Protein and DNA Encoding the Same

<130> PH-1167

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<150> JP 2000-109954

<151> 2000-04-11

<160> 28

<170> PatentIn Ver. 2.0

<210> 1

<211> 2274

<212> DNA

<213> *Xenopus laevis*

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<222> (157)..(234)

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<223> F-spondin domain

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atgaagaaag ctcattaaga acagtgggac ccagga atg gaa ctg ctc cac acc 174

Met Glu Leu Leu His Thr

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ttc tgc ggt ggg cgc tgg act ttg ctg ctc ttc acg ggg atc ttg tgc 222

Phe Cys Gly Gly Arg Trp Thr Leu Leu Leu Phe Thr Gly Ile Leu Cys

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ttt gtt gtt gcc cgc gga gtg ggg tat tat ccc agg ttc tct cca ttc 270

Phe Val Val Ala Arg Gly Val Gly Tyr Tyr Pro Arg Phe Ser Pro Phe

25

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ttt ttc ctt tgc act cat cat gga gaa ctg gaa gga gat ggg gaa caa 318  
Phe Phe Leu Cys Thr His His Gly Glu Leu Glu Gly Asp Gly Glu Gln  
40 45 50

gga gaa gtg ctc atc tct ctg cac ctg gcg ggc aac ccc agc tac tac 366  
Gly Glu Val Leu Ile Ser Leu His Leu Ala Gly Asn Pro Ser Tyr Tyr  
55 60 65 70

ata cct ggg cag gag tac cat gtg acc ata tcc act agt acc ttc ttt 414  
Ile Pro Gly Gln Glu Tyr His Val Thr Ile Ser Thr Ser Thr Phe Phe  
75 80 85

gat ggt ctt ctg gtg act gga ctt tac act tct acc agt gtt caa gcg 462  
Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser Thr Ser Val Gln Ala  
90 95 100

tct cag agc att gga ggc tct aaa gca ttt gga ttt ggt att atg agc 510  
Ser Gln Ser Ile Gly Gly Ser Lys Ala Phe Gly Phe Gly Ile Met Ser  
105 110 115

gac cgt cag ttt ggt acc cag ttt atg tgc agt gtc gtt gct tcc cac 558  
Asp Arg Gln Phe Gly Thr Gln Phe Met Cys Ser Val Val Ala Ser His  
120 125 130

gtg agt cat ctt ccc aca aca aac cta agt ttt gta tgg att gca cca 606  
Val Ser His Leu Pro Thr Thr Asn Leu Ser Phe Val Trp Ile Ala Pro  
135 140 145 150

cca gca ggt aca gga tgt gtc aac ttc atg gcc aca gca aca cat agg 654

Pro Ala Gly Thr Gly Cys Val Asn Phe Met Ala Thr Ala Thr His Arg

155

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165

gga caa gtt att ttc aag gat gcc ctg gca caa caa ctg tgc gaa caa 702

Gly Gln Val Ile Phe Lys Asp Ala Leu Ala Gln Gln Leu Cys Glu Gln

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gga gct cct act gaa gct ccc ttg cgg cct aat tta gcc gaa att cac 750

Gly Ala Pro Thr Glu Ala Pro Leu Arg Pro Asn Leu Ala Glu Ile His

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190

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agt gaa agc atc ctt tta cga gat gat ttt gac tca tat aag ctt cag 798

Ser Glu Ser Ile Leu Leu Arg Asp Asp Phe Asp Ser Tyr Lys Leu Gln

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gaa ttg aat cca aat att tgg ctc cag tgc aga aat tgc gaa gtt ggt 846

Glu Leu Asn Pro Asn Ile Trp Leu Gln Cys Arg Asn Cys Glu Val Gly

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225

230

gag cag tgt ggt gca att atg cat ggt ggg gca gtc act ttt tgt gat 894

Glu Gln Cys Gly Ala Ile Met His Gly Gly Ala Val Thr Phe Cys Asp

235

240

245

ccg tat gga cca aga gaa ttg ata act gtt caa atg aac aca act acg 942

Pro Tyr Gly Pro Arg Glu Leu Ile Thr Val Gln Met Asn Thr Thr Thr

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255

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gca tct gtt ttg cag ttt tct att ggg tca gga tcg tgc agg ttc agc 990

Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly Ser Cys Arg Phe Ser

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tat tca gac cct gga att gtg gtg tca tac aca aag aat aat tca tct			1038
Tyr Ser Asp Pro Gly Ile Val Val Ser Tyr Thr Lys Asn Asn Ser Ser			
280	285	290	
agt tgg atg cca ttg gag aga att agt gct cct tcc aat gtt agc acc			1086
Ser Trp Met Pro Leu Glu Arg Ile Ser Ala Pro Ser Asn Val Ser Thr			
295	300	305	310
atc att cac att att tac cta cct cct gaa gct aaa gga gaa aat gtg			1134
Ile Ile His Ile Ile Tyr Leu Pro Pro Glu Ala Lys Gly Glu Asn Val			
	315	320	325
aaa ttc cgt tgg agg cag gag aac atg cag gca ggt gat gtg tat gaa			1182
Lys Phe Arg Trp Arg Gln Glu Asn Met Gln Ala Gly Asp Val Tyr Glu			
	330	335	340
gcc tgc tgg gca ctg gat aac att ttg att atc aat gct gct cat aaa			1230
Ala Cys Trp Ala Leu Asp Asn Ile Leu Ile Ile Asn Ala Ala His Lys			
	345	350	355
gaa gtc gtg tta gaa gac aat cta gat cca atg gac aca gga aac tgg			1278
Glu Val Val Leu Glu Asp Asn Leu Asp Pro Met Asp Thr Gly Asn Trp			
	360	365	370
ctt ttt ttc cct ggg gct act gta aag cat acc tgt cag tcg gat gga			1326
Leu Phe Phe Pro Gly Ala Thr Val Lys His Thr Cys Gln Ser Asp Gly			
375	380	385	390

aac tct ata tat ttt cat ggt aca gaa agc agt gaa tac aac ttt gct 1374

Asn Ser Ile Tyr Phe His Gly Thr Glu Ser Ser Glu Tyr Asn Phe Ala

395

400

405

act acc aga gat gtg gat ctt tcc agt gag gac atc cag gac cag tgg 1422

Thr Thr Arg Asp Val Asp Leu Ser Ser Glu Asp Ile Gln Asp Gln Trp

410

415

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tct gaa gag ttt gag aat cta cca gct ggg taa attttagatg tagccatgag 1475

Ser Glu Glu Phe Glu Asn Leu Pro Ala Gly

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cattacattt tatcacgtga aaatgcaaga aacagtattt atatacatat tttaaaggtc 1535

aatacagaac cctataaatg gcaggttagg gctacatgt aaatatTTTT aatgttcata 1595

atgtcatagg tggtaagtat ttacatagc agttactgat tgattattat tgtttgtctt 1655

ttacccagti acagctaaca cacagggcat ttttttccaa tggcaacatc cattttgccg 1715

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taaaataaac ttcttggtta tgggtgttac catacaacac tggtaacctca tgacatatga 1835

aaaatatgac tcacattaaa tcagtaagat cagttcaagt atagtacggt gcattaatct 1895

gccaataaac atttagaatt gtattttata ttttatattt aagattagaa ttgactccat 1955

tcttgtacct tgcatcacat ttgtggctag tttatgggtc aatagacagc catcatacat 2015

tagtcagagt aaatcgagca ttacaaaact caatgagcca tagtgagtgt gacaatcaga 2075

agtgactgtc aagtaaatca accatttgct catacagatg cacatttgaa cagtggattc 2135

ttatccagaa agggccattt ttactatca ctctgggatt taaatgccac ttctaattgg 2195

aacttccagg tcacaaaaat agaatggaca tttaaacatc atggttctca ttacccttaa 2255

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<212> PRT

<213> *Xenopus laevis*

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Phe Thr Gly Ile Leu Cys Phe Val Val Ala Arg Gly Val Gly Tyr Tyr

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25

30

Pro Arg Phe Ser Pro Phe Phe Phe Leu Cys Thr His His Gly Glu Leu

35

40

45

Glu Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Leu Ala

50

55

60

Gly Asn Pro Ser Tyr Tyr Ile Pro Gly Gln Glu Tyr His Val Thr Ile

65

70

75

80

Ser Thr Ser Thr Phe Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr

85

90

95

Ser Thr Ser Val Gln Ala Ser Gln Ser Ile Gly Gly Ser Lys Ala Phe

100

105

110

Gly Phe Gly Ile Met Ser Asp Arg Gln Phe Gly Thr Gln Phe Met Cys

115

120

125

Ser Val Val Ala Ser His Val Ser His Leu Pro Thr Thr Asn Leu Ser

130

135

140

Phe Val Trp Ile Ala Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met

145

150

155

160

Ala Thr Ala Thr His Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala

165

170

175

Gln Gln Leu Cys Glu Gln Gly Ala Pro Thr Glu Ala Pro Leu Arg Pro

180

185

190

Asn Leu Ala Glu Ile His Ser Glu Ser Ile Leu Leu Arg Asp Asp Phe

195

200

205



Asp Ser Tyr Lys Leu Gln Glu Leu Asn Pro Asn Ile Trp Leu Gln Cys  
210 215 220

Arg Asn Cys Glu Val Gly Glu Gln Cys Gly Ala Ile Met His Gly Gly  
225 230 235 240

Ala Val Thr Phe Cys Asp Pro Tyr Gly Pro Arg Glu Leu Ile Thr Val  
245 250 255

Gln Met Asn Thr Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser  
260 265 270

Gly Ser Cys Arg Phe Ser Tyr Ser Asp Pro Gly Ile Val Val Ser Tyr  
275 280 285

Thr Lys Asn Asn Ser Ser Ser Trp Met Pro Leu Glu Arg Ile Ser Ala  
290 295 300

Pro Ser Asn Val Ser Thr Ile Ile His Ile Ile Tyr Leu Pro Pro Glu  
305 310 315 320

Ala Lys Gly Glu Asn Val Lys Phe Arg Trp Arg Gln Glu Asn Met Gln  
325 330 335

Ala Gly Asp Val Tyr Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Ile  
340 345 350

Ile Asn Ala Ala His Lys Glu Val Val Leu Glu Asp Asn Leu Asp Pro  
355 360 365

Met Asp Thr Gly Asn Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His  
370 375 380

Thr Cys Gln Ser Asp Gly Asn Ser Ile Tyr Phe His Gly Thr Glu Ser  
385 390 395 400

Ser Glu Tyr Asn Phe Ala Thr Thr Arg Asp Val Asp Leu Ser Ser Glu  
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Asp Ile Gln Asp Gln Trp Ser Glu Glu Phe Glu Asn Leu Pro Ala Gly  
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tcggtctccc gctaacttcc ccccgcgggc tcggttgccc ggacccgctc ggctcgagcc 180

cgccgcccggc tcgccttccc cgcacgcggc tcctccgtgc cggtgccctc gaaagtggat 240

gagagagcgc gcggggcgcg cggcgggcacg gagcgcgggc gc atg gag cgc ggc 294

Met Glu Arg Gly

1

tgc tgg gcg ccg cgg gct ctc gtc ctg gcc gtg ctg ctg ctg ctg gcg 342

Cys Trp Ala Pro Arg Ala Leu Val Leu Ala Val Leu Leu Leu Leu Ala

5

10

15

20

acg ctg agg gcg cgc gcg gcc acc ggc tac tac ccg cgc ttc tcg cct 390

Thr Leu Arg Ala Arg Ala Ala Thr Gly Tyr Tyr Pro Arg Phe Ser Pro

25

30

35

ttc ttt ttc ctg tgc acc cac cac ggg gag ctg gaa ggg gat ggg gag 438  
Phe Phe Phe Leu Cys Thr His His Gly Glu Leu Glu Gly Asp Gly Glu  
40 45 50

cag ggc gag gtg ctc att tcc ctg cac att gcg ggc aac ccc acc tac 486  
Gln Gly Glu Val Leu Ile Ser Leu His Ile Ala Gly Asn Pro Thr Tyr  
55 60 65

tac gta ccg gga cag gaa tac cat gtt aca att tca aca agc acc ttc 534  
Tyr Val Pro Gly Gln Glu Tyr His Val Thr Ile Ser Thr Ser Thr Phe  
70 75 80

ttt gat ggc ttg ctg gtg acg gga ctc tat acc tcg aca agc atc cag 582  
Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser Thr Ser Ile Gln  
85 90 95 100

tct tct cag agc att gga ggc tcc agc gcc ttt gga ttc ggg atc atg 630  
Ser Ser Gln Ser Ile Gly Gly Ser Ser Ala Phe Gly Phe Gly Ile Met  
105 110 115

tcc gac cac cag ttt ggt aac cag ttt atg tgc agt gtg gtg gcc tct 678  
Ser Asp His Gln Phe Gly Asn Gln Phe Met Cys Ser Val Val Ala Ser  
120 125 130

cat gtg agt cac ctg cct aca acc aac ctc agc ttt gtc tgg att gcc 726  
His Val Ser His Leu Pro Thr Thr Asn Leu Ser Phe Val Trp Ile Ala  
135 140 145

cca cca gct ggc aca ggc tgt gtg aat ttc atg gct act gca aca cat 774

Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met Ala Thr Ala Thr His  
 150 155 160

agg ggc cag gtg att ttc aaa gac gca ctg gcc cag cag ctg tgt gaa 822  
 Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala Gln Gln Leu Cys Glu  
 165 170 175 180

caa gga gct ccc aca gag gcc act gct tac tcg cac ctt gct gaa ata 870  
 Gln Gly Ala Pro Thr Glu Ala Thr Ala Tyr Ser His Leu Ala Glu Ile  
 185 190 195

cac agt gac agt gtg atc cta cga gat gac ttt gac tcc tac cag caa 918  
 His Ser Asp Ser Val Ile Leu Arg Asp Asp Phe Asp Ser Tyr Gln Gln  
 200 205 210

ctg gaa ttg aac ccc aac ata tgg gtt gaa tgc agc aac tgt gag atg 966  
 Leu Glu Leu Asn Pro Asn Ile Trp Val Glu Cys Ser Asn Cys Glu Met  
 215 220 225

gga gag cag tgt ggc acc atc atg cat ggc aat gct gtc acc ttc tgt 1014  
 Gly Glu Gln Cys Gly Thr Ile Met His Gly Asn Ala Val Thr Phe Cys  
 230 235 240

gag ccg tac ggc cct cga gag ctg acc acc aca tgc ctg aac aca aca 1062  
 Glu Pro Tyr Gly Pro Arg Glu Leu Thr Thr Thr Cys Leu Asn Thr Thr  
 245 250 255 260

aca gca tct gtc ctc cag ttt tcc att ggg tca gga tca tgt cga ttt 1110  
 Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly Ser Cys Arg Phe

265	270	275	
agt tac tct gac ccc agc atc act gtg tca tac gcc aag aac aat acc			1158
Ser Tyr Ser Asp Pro Ser Ile Thr Val Ser Tyr Ala Lys Asn Asn Thr			
280	285	290	
gct gat tgg att cag ctg gag aaa att aga gcc cct tcc aat gtg agc			1206
Ala Asp Trp Ile Gln Leu Glu Lys Ile Arg Ala Pro Ser Asn Val Ser			
295	300	305	
aca gtc atc cac atc ctg tac ctc ccc gag gaa gcc aaa ggg gag agc			1254
Thr Val Ile His Ile Leu Tyr Leu Pro Glu Glu Ala Lys Gly Glu Ser			
310	315	320	
gtg cag ttc cag tgg aaa cag gac agc ctg cga gtg ggt gag gtg tat			1302
Val Gln Phe Gln Trp Lys Gln Asp Ser Leu Arg Val Gly Glu Val Tyr			
325	330	335	340
gag gcc tgc tgg gcc ctg gat aac atc ctg gtc atc aat tca gcc cac			1350
Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Val Ile Asn Ser Ala His			
345	350	355	
aga gaa gtc gtt ctg gag gac aac ctc gac ccg gtc gac acg ggc aac			1398
Arg Glu Val Val Leu Glu Asp Asn Leu Asp Pro Val Asp Thr Gly Asn			
360	365	370	
tgg ctc ttc ttc cct gga gca acg gtc aag cat agc tgt cag tca gat			1446
Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His Ser Cys Gln Ser Asp			
375	380	385	

ggg aac tcc att tat ttc cat gga aat gaa ggc agc gag ttc aat ttt 1494  
 Gly Asn Ser Ile Tyr Phe His Gly Asn Glu Gly Ser Glu Phe Asn Phe  
 390 395 400

gcc acc acc cgg gat gta gat ctt tct aca gag gat att caa gag cag 1542  
 Ala Thr Thr Arg Asp Val Asp Leu Ser Thr Glu Asp Ile Gln Glu Gln  
 405 410 415 420

tgg tca gaa gaa ttt gag agc cag ccc aca gga tgg gat atc ttg gga 1590  
 Trp Ser Glu Glu Phe Glu Ser Gln Pro Thr Gly Trp Asp Ile Leu Gly  
 425 430 435

gca gta gtt ggt gca gac tgt gga acc gta gaa tca gga cta tca ctg 1638  
 Ala Val Val Gly Ala Asp Cys Gly Thr Val Glu Ser Gly Leu Ser Leu  
 440 445 450

gtg ttc ctc aaa gat gga gag agg aag ctt tgc acc ccc tac atg gat 1686  
 Val Phe Leu Lys Asp Gly Glu Arg Lys Leu Cys Thr Pro Tyr Met Asp  
 455 460 465

aca act ggt tat ggc aac ctg agg ttc tac ttc gtt atg gga gga atc 1734  
 Thr Thr Gly Tyr Gly Asn Leu Arg Phe Tyr Phe Val Met Gly Gly Ile  
 470 475 480

tgt gac cct gga gtc tct cat gaa aac gat atc atc tta tat gca aag 1782  
 Cys Asp Pro Gly Val Ser His Glu Asn Asp Ile Ile Leu Tyr Ala Lys  
 485 490 495 500

att gaa gga aga aaa gaa cac att gca ctg gac act ctt acc tat tct 1830  
 Ile Glu Gly Arg Lys Glu His Ile Ala Leu Asp Thr Leu Thr Tyr Ser  
 505 510 515

tcc tat aag gtt ccg tct ttg gtt tct gtg gtc atc aac cct gaa ctt 1878  
 Ser Tyr Lys Val Pro Ser Leu Val Ser Val Val Ile Asn Pro Glu Leu  
 520 525 530

cag aca cct gcc acc aaa ttt tgt ctc agg caa aag agc cac caa ggg 1926  
 Gln Thr Pro Ala Thr Lys Phe Cys Leu Arg Gln Lys Ser His Gln Gly  
 535 540 545

tat aat cgg aat gtc tgg gct gtg gac ttc ttc cat gtg ctg ccc gtt 1974  
 Tyr Asn Arg Asn Val Trp Ala Val Asp Phe Phe His Val Leu Pro Val  
 550 555 560

ctc cct tca aca atg tct cac atg atc cag ttt tct att aat ttg gga 2022  
 Leu Pro Ser Thr Met Ser His Met Ile Gln Phe Ser Ile Asn Leu Gly  
 565 570 575 580

tgc ggc aca cac cag cct ggg aac agg tga gaagcatgcc gagtgccta 2072  
 Cys Gly Thr His Gln Pro Gly Asn Arg  
 585 590

acatggtagg aaataaacac atgcactgga ccattgaagt aagtttgtca gtaggatttt 2132

tggatgggat tttaacaaaa tatccattaa gaaaatacag attcctactc cctccctaaa 2192

agagttcittt ggtaataaaa tagaagggat gtgactgggt agatttttag gttagaatag 2252



tttcattcag ggagcttgat acaagttatc agagggtgtc accatgctgt gtggcagcat 2312

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gctcctcttg cataagtgtt gctcccatcc tctgtaaaga actttgctga cctcacattc 2492

acaggatgaa gtgacagtgt gagacatggt aattgcctag ctatctatca aattcaagag 2552

cacaaaccca gtttactgtg tattgtcctt cagacgtagc ttttatggca gtaatccaat 2612

ggcttgccct ctgaaggctg gtcaggcttc agtgagagat gacacattta gtaaaggctt 2672

tagagaaatc ccacattcat cgactcattc aaggatattta gctagaaata aaaagaatca 2732

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<213> Mus musculus

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Arg Phe Ser Pro Phe Phe Phe Leu Cys Thr His His Gly Glu Leu Glu  
35 40 45

Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Ile Ala Gly  
50 55 60

Asn Pro Thr Tyr Tyr Val Pro Gly Gln Glu Tyr His Val Thr Ile Ser  
65 70 75 80

Thr Ser Thr Phe Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser  
85 90 95

Thr Ser Ile Gln Ser Ser Gln Ser Ile Gly Gly Ser Ser Ala Phe Gly  
100 105 110

Phe Gly Ile Met Ser Asp His Gln Phe Gly Asn Gln Phe Met Cys Ser  
115 120 125

Val Val Ala Ser His Val Ser His Leu Pro Thr Thr Asn Leu Ser Phe  
130 135 140

Val Trp Ile Ala Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met Ala  
145 150 155 160

Thr Ala Thr His Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala Gln  
165 170 175

Gln Leu Cys Glu Gln Gly Ala Pro Thr Glu Ala Thr Ala Tyr Ser His  
180 185 190

Leu Ala Glu Ile His Ser Asp Ser Val Ile Leu Arg Asp Asp Phe Asp  
195 200 205

Ser Tyr Gln Gln Leu Glu Leu Asn Pro Asn Ile Trp Val Glu Cys Ser  
210 215 220

Asn Cys Glu Met Gly Glu Gln Cys Gly Thr Ile Met His Gly Asn Ala  
225 230 235 240

Val Thr Phe Cys Glu Pro Tyr Gly Pro Arg Glu Leu Thr Thr Thr Cys  
245 250 255

Leu Asn Thr Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly  
260 265 270

Ser Cys Arg Phe Ser Tyr Ser Asp Pro Ser Ile Thr Val Ser Tyr Ala  
275 280 285

Lys Asn Asn Thr Ala Asp Trp Ile Gln Leu Glu Lys Ile Arg Ala Pro  
290 295 300

Ser Asn Val Ser Thr Val Ile His Ile Leu Tyr Leu Pro Glu Glu Ala  
305 310 315 320

Lys Gly Glu Ser Val Gln Phe Gln Trp Lys Gln Asp Ser Leu Arg Val

	325		330		335										
Gly	Glu	Val	Tyr	Glu	Ala	Cys	Trp	Ala	Leu	Asp	Asn	Ile	Leu	Val	Ile
	340		345		350										
Asn	Ser	Ala	His	Arg	Glu	Val	Val	Leu	Glu	Asp	Asn	Leu	Asp	Pro	Val
	355		360		365										
Asp	Thr	Gly	Asn	Trp	Leu	Phe	Phe	Pro	Gly	Ala	Thr	Val	Lys	His	Ser
	370		375		380										
Cys	Gln	Ser	Asp	Gly	Asn	Ser	Ile	Tyr	Phe	His	Gly	Asn	Glu	Gly	Ser
385			390		395									400	
Glu	Phe	Asn	Phe	Ala	Thr	Thr	Arg	Asp	Val	Asp	Leu	Ser	Thr	Glu	Asp
		405			410									415	
Ile	Gln	Glu	Gln	Trp	Ser	Glu	Glu	Phe	Glu	Ser	Gln	Pro	Thr	Gly	Trp
	420		425		430										
Asp	Ile	Leu	Gly	Ala	Val	Val	Gly	Ala	Asp	Cys	Gly	Thr	Val	Glu	Ser
	435		440		445										
Gly	Leu	Ser	Leu	Val	Phe	Leu	Lys	Asp	Gly	Glu	Arg	Lys	Leu	Cys	Thr
	450		455		460										
Pro	Tyr	Met	Asp	Thr	Thr	Gly	Tyr	Gly	Asn	Leu	Arg	Phe	Tyr	Phe	Val
465			470		475									480	

Met Gly Gly Ile Cys Asp Pro Gly Val Ser His Glu Asn Asp Ile Ile

485

490

495

Leu Tyr Ala Lys Ile Glu Gly Arg Lys Glu His Ile Ala Leu Asp Thr

500

505

510

Leu Thr Tyr Ser Ser Tyr Lys Val Pro Ser Leu Val Ser Val Val Ile

515

520

525

Asn Pro Glu Leu Gln Thr Pro Ala Thr Lys Phe Cys Leu Arg Gln Lys

530

535

540

Ser His Gln Gly Tyr Asn Arg Asn Val Trp Ala Val Asp Phe Phe His

545

550

555

560

Val Leu Pro Val Leu Pro Ser Thr Met Ser His Met Ile Gln Phe Ser

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Ile Asn Leu Gly Cys Gly Thr His Gln Pro Gly Asn Arg

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

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<400> 5

arttyggnaa ycarttyatg tg

22

<210> 6

<211> 16

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:synthetic DNA

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16

<210> 7

<211> 20

<212> DNA

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<223> Description of Artificial Sequence:synthetic DNA

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<210> 8

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<212> DNA

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<223> Description of Artificial Sequence:synthetic DNA

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